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Article on Information Technology

U.S. biotechnology information center adds new standard submission format for its Trace Archive

2006 FEB 27 -- 454 Life Sciences Corporation announced that the U.S. National Center for Biotechnology Information (NCBI) has added a new standard submission format for its Trace Archive of sequencing data.

Data generated with 454 Life Sciences' technology can now be directly entered into the Trace Archive. Sequence trace data generated with 454 Life Sciences' technology is submitted in a newly created format called standard flowgram format (SFF) and represents the first new sequence trace format adopted by the NCBI since the Sanger method.

"The submission of our sequencing data allowed for the results to be publicly available prior to the publication of our article in the peer-reviewed journal, *Science*," stated Stephan C. Schuster, associate professor at Penn State's Center for Comparative Genomics and Bioinformatics.

The Trace Archive (in collaboration with the Ensembl Trace Server) is a repository for the raw sequence data underlying genome projects. Although the initial data deposition to this repository occurred in early 2001, the content of the repository is rapidly approaching 1,000,000,000 traces representing over 480 species. The Trace Archive has become crucial in the storage, management and dissemination of sequence data.

The U.S. National Center for Biotechnology Information (NCBI) is a division of the U.S. National Library of Medicine (NLM) at the U.S. National Institutes of Health (NIH). As a national resource for molecular biology information, NCBI's mission is to develop new information technologies to aid in the understanding of fundamental molecular and genetic processes that control health and disease.

454 Life Sciences, a 66% majority-owned subsidiary of CuraGen Corporation (CRGN), is commercializing novel instrumentation and measurement services for conducting high-throughput nucleotide sequencing, with specific application to sequencing of whole genomes and ultra-deep sequencing of target genes.